

SEQUENCE LISTING

<110> Bartha, Gabor
Walker, Michael

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METHODS FOR ANALYZING GENE EXPRESSION PATTERNS

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<151> 2000-11-01

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Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
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Gly Gln Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Lys Lys Ile
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 ctgccaatca gcattctcatt gtgcaggatc tgggtgaacat cggggcacag gtgaacacca 720
 cagactgctg ggggaagaaca cctctgcatg tgtgtgctga gaagggccac tcccagggtgc 780
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 aactccagag aaatcaacag cctcattcac ctgaagttca ggagctttta ctgaagaata 960
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 cttacaatgg caacactgcc ctccatgttg ctgccagctt gcagtatcgg ttgacacaat 1080
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<210> 8
 <211> 402
 <212> PRT
 <213> Human

<400> 8
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 Val Glu Gln Gln Pro His Tyr Thr His Lys Pro Thr Leu Glu Tyr Ser
 20 25 30
 Pro Phe Pro Ile Pro Pro Gln Ser Pro Ala Tyr Glu Pro Asn Leu Phe
 35 40 45
 Asp Gly Pro Glu Ser Gln Phe Cys Pro Asn Gln Ser Leu Val Ser Leu
 50 55 60
 Leu Gly Asp Gln Arg Glu Ser Glu Asn Ile Ala Asn Pro Met Gln Thr
 65 70 75 80
 Ser Ser Ser Val Gln Gln Asn Asp Ala His Leu His Ser Phe Ser
 85 90 95
 Met Met Pro Ser Ser Ala Cys Glu Ala Met Val Gly His Glu Met Ala
 100 105 110
 Ser Asp Ser Ser Asn Thr Ser Leu Pro Phe Ser Asn Met Gly Asn Pro
 115 120 125

Met	Asn	Thr	Thr	Gln	Leu	Gly	Lys	Ser	Leu	Phe	Gln	Trp	Gln	Val	Glu
130						135					140				
Gln	Glu	Glu	Ser	Lys	Leu	Ala	Asn	Ile	Ser	Gln	Asp	Gln	Phe	Leu	Ser
145					150					155					160
Lys	Asp	Ala	Asp	Gly	Asp	Thr	Phe	Leu	His	Ile	Ala	Val	Ala	Gln	Gly
				165					170					175	
Arg	Arg	Ala	Leu	Ser	Tyr	Val	Leu	Ala	Arg	Lys	Met	Asn	Ala	Leu	His
			180					185					190		
Met	Leu	Asp	Ile	Lys	Glu	His	Asn	Gly	Gln	Ser	Ala	Phe	Gln	Val	Ala
		195					200					205			
Val	Ala	Ala	Asn	Gln	His	Leu	Ile	Val	Gln	Asp	Leu	Val	Asn	Ile	Gly
		210				215					220				
Ala	Gln	Val	Asn	Thr	Thr	Asp	Cys	Trp	Gly	Arg	Thr	Pro	Leu	His	Val
225					230					235					240
Cys	Ala	Glu	Lys	Gly	His	Ser	Gln	Val	Leu	Gln	Ala	Ile	Gln	Lys	Gly
				245					250					255	
Ala	Val	Gly	Ser	Asn	Gln	Phe	Val	Asp	Leu	Glu	Ala	Thr	Asn	Tyr	Asp
			260					265					270		
Gly	Leu	Thr	Pro	Leu	His	Cys	Ala	Val	Ile	Ala	His	Asn	Ala	Val	Val
		275				280						285			
His	Glu	Leu	Gln	Arg	Asn	Gln	Gln	Pro	His	Ser	Pro	Glu	Val	Gln	Glu
		290				295					300				
Leu	Leu	Leu	Lys	Asn	Lys	Ser	Leu	Val	Asp	Thr	Ile	Lys	Cys	Leu	Ile
305					310					315					320
Gln	Met	Gly	Ala	Ala	Val	Glu	Ala	Lys	Ala	Tyr	Asn	Gly	Asn	Thr	Ala
				325					330					335	
Leu	His	Val	Ala	Ala	Ser	Leu	Gln	Tyr	Arg	Leu	Thr	Gln	Leu	Asp	Ala
			340					345					350		
Val	Arg	Leu	Leu	Met	Arg	Lys	Gly	Ala	Asp	Pro	Ser	Thr	Arg	Asn	Leu
		355					360					365			
Glu	Asn	Glu	Gln	Pro	Val	His	Leu	Val	Pro	Asp	Gly	Pro	Val	Gly	Glu
		370				375					380				
Gln	Ile	Arg	Arg	Ile	Leu	Lys	Gly	Lys	Ser	Ile	Gln	Gln	Arg	Ala	Pro
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Pro	Tyr														

<210> 9
 <211> 1057
 <212> DNA
 <213> Human

<400> 9
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 gaggccacct ggattgtgcc taatgtgttt gagcatcgct taggagaagt cttctattta 540
 tttatttatt cattagtttt gaagattcta tgtaaatatt ttaggtgtaa aataattaag 600
 ggtatgatta actctacctg cacactgtcc tatttatattc attctttttg aaatgtcaac 660


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ctggcggatc caagcaaattg gccaatgaga tcattgtgaa ggcaggggaa tgtatgtgca 840
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tgtgtggtca acatttctca tgttgaaact ttaagaacta aaatgttcta aatatccctt 960
ggacatttta tgtctttctt gtaaggcata ctgccttggt taatggtagt tttacagtgt 1020
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<210> 10
<211> 107
<212> PRT
<213> Human

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          20          25          30
Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
          35          40          45
Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser
          50          55          60
Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
65          70          75          80
Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile
          85          90          95
Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn
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<210> 11
<211> 794
<212> DNA
<213> Human

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<220>
<221> misc_feature
<222> 7, 14, 22, 35, 37
<223> n = A,T,C or G

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<221> misc_feature
<222> 7, 14, 22, 35, 37
<223> n = A,T,C or G

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<400> 11
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gatataattta caggctgggt caggactatc tgcagtgagt cctacagata ccacaacctg 180
gatcagggtcc aagcaaaacg tccagagtgct taaaaaatgt tgcgtttctca gtccaaaaag 240
aagtggaaaa gaatctgaag tcatgcttggt acaatgttaa tgttgtgtcc gtagacactg 300
ccagaacact attcaaccaa gtgatggaaa aggagtttga agacgacatc attaactggg 360
gaagaattgt aacctatatt gcatttgaag gtattctcat caagaaactt ctacgacagc 420
aaattgcccc ggatgtggat acctataagg agatttcata ttttggttgcg gagttcataa 480
tgaataacac aggagaatgg ataaggcaaa acggaggctg ggaaaatggc tttgtaaaga 540
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<210> 14
 <211> 81
 <212> PRT
 <213> Human

<400> 14
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 20 25 30
 Ser Gly Arg Arg Thr Arg Leu Cys Cys His Arg Val Pro Ser Pro Asn
 35 40 45
 Ser Thr Asn Leu Lys Gly His His Val Arg Leu Cys Lys Pro Cys Lys
 50 55 60
 Leu Glu Pro Glu Pro Arg Leu Trp Val Val Pro Gly Ala Leu Pro Gln
 65 70 75 80
 Val

<210> 15
 <211> 3169
 <212> DNA
 <213> Human

<400> 15
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 gatattgtca ttgttataga tcctagtgtg ccagaagatg aaaaaataat tgaacaaata 180
 gaggatatgg tgactacagc ttctacgtac ctgtttgaag ccacagaaaa aagatttttt 240
 ttcaaaaatg tatctatatt aattcctgag aattggaagg aaaatcctca gtacaaaagg 300
 ccaaaacatg aaaaccataa acatgctgat gttatagttg caccacctac actcccagg 360
 agagatgaac catacaccaa gcagttcaca gaatgtggag agaaaggcga atacattcac 420
 ttcaccctctg accttctact tggaaaaaaa caaaatgaat atggaccacc aggcaactg 480
 tttgtccatg agtgggctca cctccggtgg ggagtgtttg atgagtacaa tgaagatcag 540
 cctttctacc gtgctaagtc aaaaaaaatc gaagcaacaa ggtgttccgc aggtatctct 600
 ggtagaaata gagtttataa gtgtcaagga ggcagctgtc ttagtagagc atgcagaatt 660
 gattctacaa caaaactgta tggaaaagat tgtcaattct ttcttgataa agtacaaaca 720
 gaaaaagcat ccataatgtt tatgcaaagt attgattctg ttgttgaatt ttgtaacgaa 780
 aaaaccata atcaagaagc tccaagccta caaaacataa agtgcaattt tagaagtaca 840
 tgggaggtga ttagcaattc tgaggatttt aaaaacacca taccatggg gacaccacct 900
 cctccacctg tcttctcatt gctgaagatc agtcaaaaga ttgtgtgctt agttcttgat 960
 aagtctggaa gcatgggggg taaggaccgc ctaaatcgaa tgaatcaagc agcaaaacat 1020
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 gcaggattac ctacatatcc tctgggagga acttccatct gctctggaat taaatatgca 1200
 tttcaggtga ttggagagct acattcccaa ctcgatggat ccgaagtact gctgctgact 1260
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			180				185				190				
Gly	Arg		Arg	Val	Tyr	Lys	Cys	Gln	Gly	Gly	Ser	Cys	Leu	Ser	Arg
			195				200				205				
Ala	Cys	Arg	Ile	Asp	Ser	Thr	Thr	Lys	Leu	Tyr	Gly	Lys	Asp	Cys	Gln
			210				215				220				
Phe	Phe	Pro	Asp	Lys	Val	Gln	Thr	Glu	Lys	Ala	Ser	Ile	Met	Phe	Met
225				230				235				240			
Gln	Ser	Ile	Asp	Ser	Val	Val	Glu	Phe	Cys	Asn	Glu	Lys	Thr	His	Asn
			245				250				255				
Gln	Glu	Ala	Pro	Ser	Leu	Gln	Asn	Ile	Lys	Cys	Asn	Phe	Arg	Ser	Thr
			260				265				270				
Trp	Glu	Val	Ile	Ser	Asn	Ser	Glu	Asp	Phe	Lys	Asn	Thr	Ile	Pro	Met
			275				280				285				
Val	Thr	Pro	Pro	Pro	Pro	Pro	Val	Phe	Ser	Leu	Leu	Lys	Ile	Ser	Gln
			290				295				300				
Arg	Ile	Val	Cys	Leu	Val	Leu	Asp	Lys	Ser	Gly	Ser	Met	Gly	Gly	Lys
305				310				315				320			
Asp	Arg	Leu	Asn	Arg	Met	Asn	Gln	Ala	Ala	Lys	His	Phe	Leu	Leu	Gln
			325				330				335				
Thr	Val	Glu	Asn	Gly	Ser	Trp	Val	Gly	Met	Val	His	Phe	Asp	Ser	Thr
			340				345				350				
Ala	Thr	Ile	Val	Asn	Lys	Leu	Ile	Gln	Ile	Lys	Ser	Ser	Asp	Glu	Arg
			355				360				365				
Asn	Thr	Leu	Met	Ala	Gly	Leu	Pro	Thr	Tyr	Pro	Leu	Gly	Gly	Thr	Ser
			370				375				380				
Ile	Cys	Ser	Gly	Ile	Lys	Tyr	Ala	Phe	Gln	Val	Ile	Gly	Glu	Leu	His
385				390				395				400			
Ser	Gln	Leu	Asp	Gly	Ser	Glu	Val	Leu	Leu	Leu	Thr	Asp	Gly	Glu	Asp
			405				410				415				
Asn	Thr	Ala	Ser	Ser	Cys	Ile	Asp	Glu	Val	Lys	Gln	Ser	Gly	Ala	Ile
			420				425				430				
Val	His	Phe	Ile	Ala	Leu	Gly	Arg	Ala	Ala	Asp	Glu	Ala	Val	Ile	Glu
			435				440				445				
Met	Ser	Lys	Ile	Thr	Gly	Gly	Ser	His	Phe	Tyr	Val	Ser	Asp	Glu	Ala
			450				455				460				
Gln	Asn	Asn	Gly	Leu	Ile	Asp	Ala	Phe	Gly	Ala	Leu	Thr	Ser	Gly	Asn
465				470				475				480			
Thr	Asp	Leu	Ser	Gln	Lys	Ser	Leu	Gln	Leu	Glu	Ser	Lys	Gly	Leu	Thr
			485				490				495				
Leu	Asn	Ser	Asn	Ala	Trp	Met	Asn	Asp	Thr	Val	Ile	Ile	Asp	Ser	Thr
			500				505				510				
Val	Gly	Lys	Asp	Thr	Phe	Phe	Leu	Ile	Thr	Trp	Asn	Ser	Leu	Pro	Pro
			515				520				525				
Ser	Ile	Ser	Leu	Trp	Asp	Pro	Ser	Gly	Thr	Ile	Met	Glu	Asn	Phe	Thr
			530				535				540				
Val	Asp	Ala	Thr	Ser	Lys	Met	Ala	Tyr	Leu	Ser	Ile	Pro	Gly	Thr	Ala
545				550				555				560			
Lys	Val	Gly	Thr	Trp	Ala	Tyr	Asn	Leu	Gln	Ala	Lys	Ala	Asn	Pro	Glu
			565				570				575				
Thr	Leu	Thr	Ile	Thr	Val	Thr	Ser	Arg	Ala	Ala	Asn	Ser	Ser	Val	Pro
			580				585				590				


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cactgggatg tttacccac tagctgcagc agatgctgag cctcctctcc ttggcagggg 660
cactgtgatg aggagtaaga actcccttat cactaaccac catccaaatg gctcaataaa 720
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<210> 18
<211> 198
<212> PRT
<213> Human

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<400> 18
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Lys Phe Pro Gly Gly Cys Phe Ala Ser Glu Thr Val Ser Pro Arg Met
          20           25           30
Leu Thr Val Ala Leu Leu Ala Leu Leu Cys Ala Ser Ala Ser Gly Asn
          35           40           45
Ala Ile Gln Ala Arg Ser Ser Ser Tyr Ser Gly Glu Tyr Gly Ser Gly
          50           55           60
Gly Gly Lys Arg Phe Ser His Ser Gly Asn Gln Leu Asp Gly Pro Ile
65           70           75           80
Thr Ala Leu Arg Val Arg Val Asn Thr Tyr Tyr Ile Val Gly Leu Gln
          85           90           95
Val Arg Tyr Gly Lys Val Trp Ser Asp Tyr Val Gly Gly Arg Asn Gly
          100          105          110
Asp Leu Glu Glu Ile Phe Leu His Pro Gly Glu Ser Val Ile Gln Val
          115          120          125
Ser Gly Lys Tyr Lys Trp Tyr Leu Lys Lys Leu Val Phe Val Thr Asp
          130          135          140
Lys Gly Arg Tyr Leu Ser Phe Gly Lys Asp Ser Gly Thr Ser Phe Asn
145          150          155          160
Ala Val Pro Leu His Pro Asn Thr Val Leu Arg Phe Ile Ser Gly Arg
          165          170          175
Ser Gly Ser Leu Ile Asp Ala Ile Gly Leu His Trp Asp Val Tyr Pro
          180          185          190
Thr Ser Cys Ser Arg Cys
          195

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<210> 19
<211> 2879
<212> DNA
<213> Human

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<400> 19
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aagaagtgtt caccacatag ttgcaaaggc cttcaacttg ccacagccaa cagaaaaatc 180
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gcagtttcag	gagcagtttc	aaaagcagtc	ccagatcgca	atgcaactac	tttgggattg	660
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aaaacaactt	tatacccaga	aagtatttga	taagttcata	cattgtacga	agagtatttt	2580
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<210>	20
<211>	764
<212>	PRT
<213>	Human

<400> 20															
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Asn Val Thr Val Leu Val Ala Ser Gly Ala Leu Phe Ile Thr Pro Thr
          50          55          60
Ser Asn Pro Ser Leu Thr Phe Glu Ile Tyr Lys Val Pro Phe Gly Lys
65          70          75          80
Glu Arg Ile Glu Gly Val Ile Lys Asp Phe Val Leu Thr Trp Leu Glu
          85          90          95
Asn Arg Pro Ser Pro Ser Thr Ile Trp Arg Phe Tyr Gln Glu Met Ala
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Val	Cys	Val	Thr	Thr	Ala	Ile	Phe	Leu	Val	Ile	Gln	Cys	Cys	Leu	Phe		
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Val Tyr Ile Gln Gly Val Ala Ser Glu His Met Lys Arg Phe Phe Val
 35          40          45
Asn Phe Val Val Gly Gln Asp Pro Gly Ser Asp Val Ala Phe His Phe
 50          55          60
Asn Pro Arg Phe Asp Gly Trp Asp Lys Val Val Phe Asn Thr Leu Gln
 65          70          75          80
Gly Gly Lys Trp Gly Ser Glu Glu Arg Lys Arg Ser Met Pro Phe Lys
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Pro	Leu	Gln	Met	Val	Thr	His	Leu	Gln	Val	Asp	Gly	Asp	Leu	Gln	Leu		
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Gln	Ser	Ile	Asn	Phe	Ile	Gly	Gly	Gln	Pro	Leu	Arg	Pro	Gln	Gly	Pro		
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Pro	Met	Met	Pro	Pro	Tyr	Pro	Gly	Pro	Gly	His	Cys	His	Gln	Gln	Leu		
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Ile	Ile	Lys	Gly	Tyr	Val	Pro	Pro	Thr	Gly	Lys	Ser	Phe	Ala	Ile	Asn		
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Phe	Lys	Val	Gly	Ser	Ser	Gly	Asp	Ile	Ala	Leu	His	Ile	Asn	Pro	Arg		
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Gln	Arg	Val	Asp	Thr	Leu	Glu	Ile	Gln	Gly	Asp	Val	Thr	Leu	Ser	Tyr		
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